

Fig A. Sensitivity of the prediction for different fetal fraction and microdeletion size.

Read count was set to 20M in each sample. Detections 2Mb away from critical region are reported.

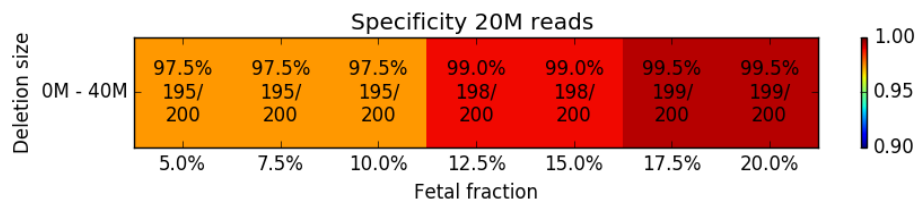


Fig B. Specificity of the prediction for different fetal fraction and microdeletion size.

Read count was set to 20M in each sample. Detections 2Mb away from critical region are reported.

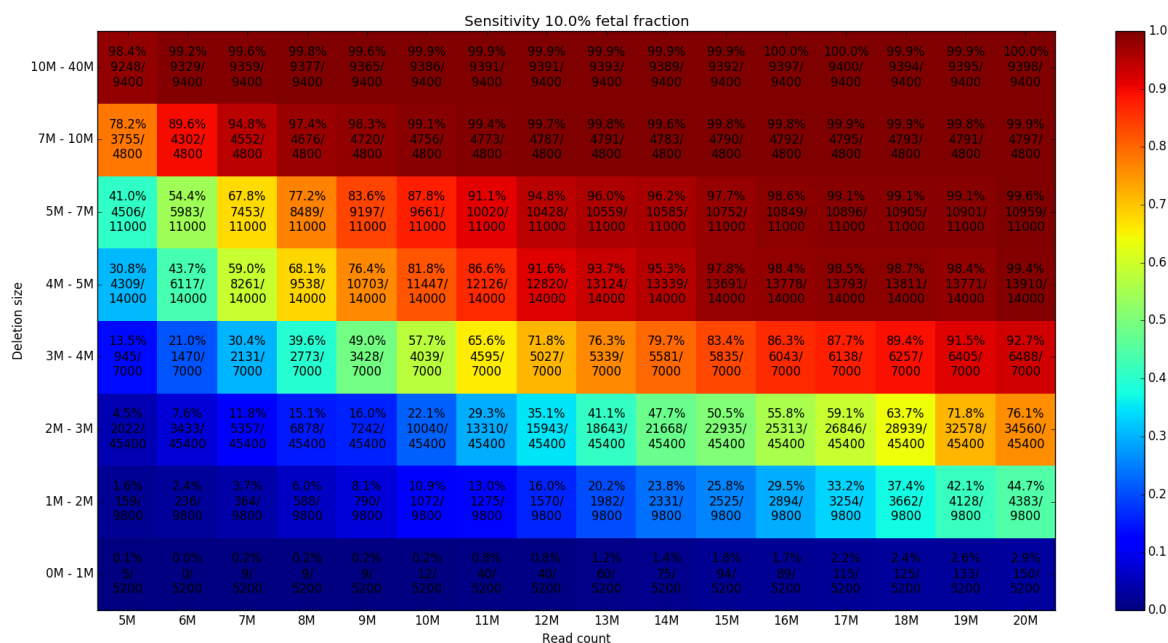


Fig C. Sensitivity of the prediction for different read count and microdeletion size.

Fetal fraction was set to 10% for all samples. Detections 2Mb away from critical region are reported.

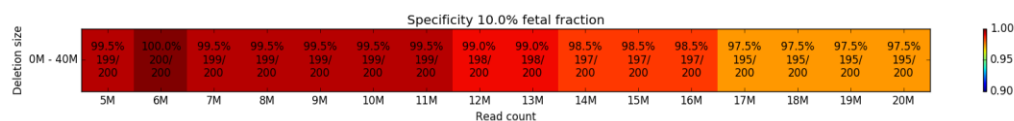


Fig D. Specificity of the prediction for different read count and microdeletion size.

Fetal fraction was set to 10% for all samples. Detections 2Mb away from critical region are reported.

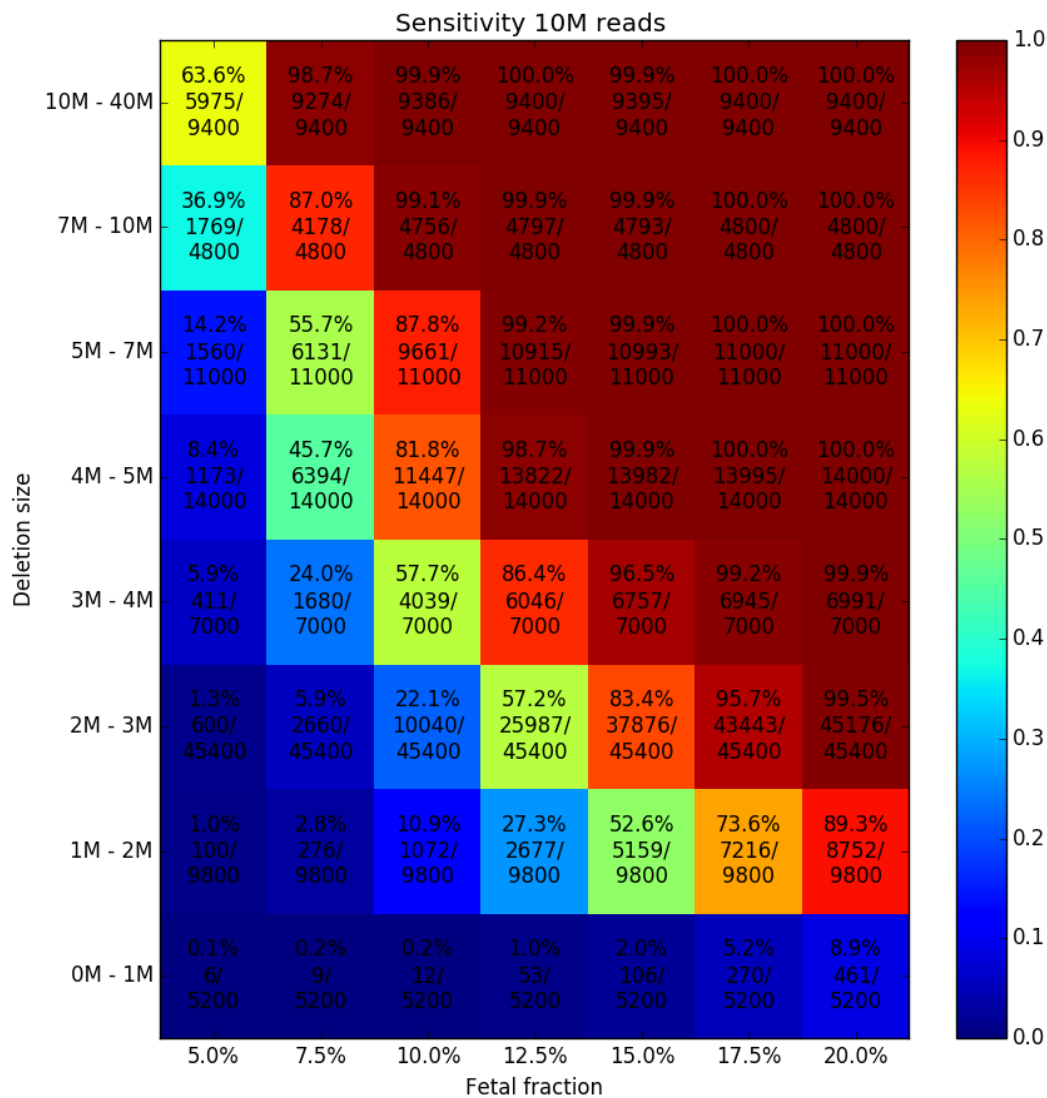


Fig E. Sensitivity of the prediction for different fetal fraction and microdeletion size.

Read count was set to 10M in each sample. Detections 2Mb away from critical region are reported.

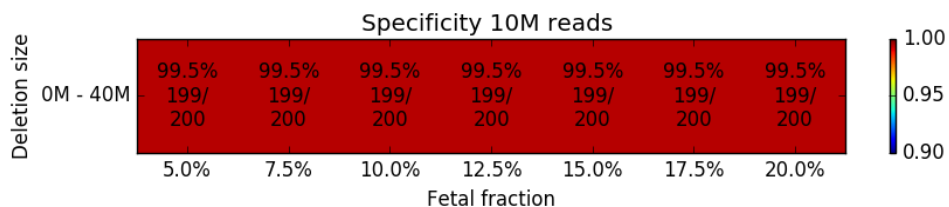


Fig F. Specificity of the prediction for different fetal fraction and microdeletion size.

Read count was set to 10M in each sample. Detections 2Mb away from critical region are reported.

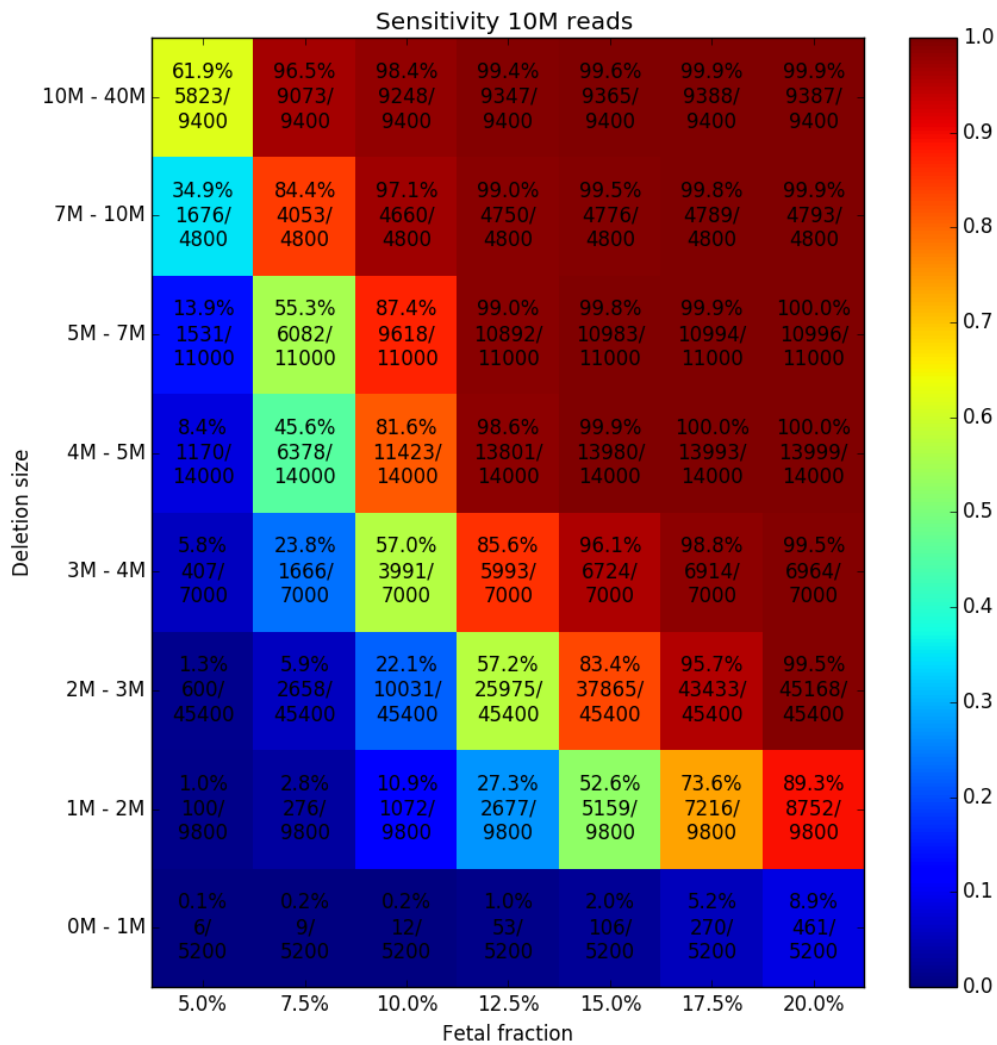


Fig G. Sensitivity of the prediction for different fetal fraction and microdeletion size.

Read count was set to 10M in each sample. Detections 2Mb away from critical region are NOT reported.

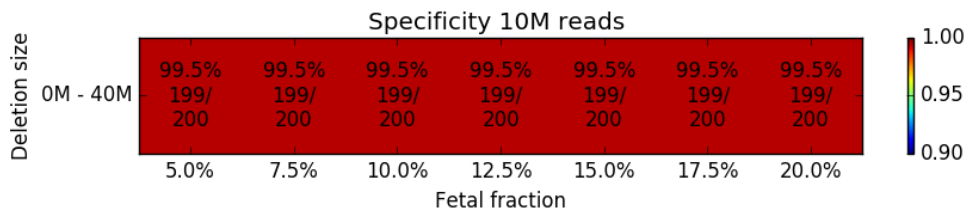
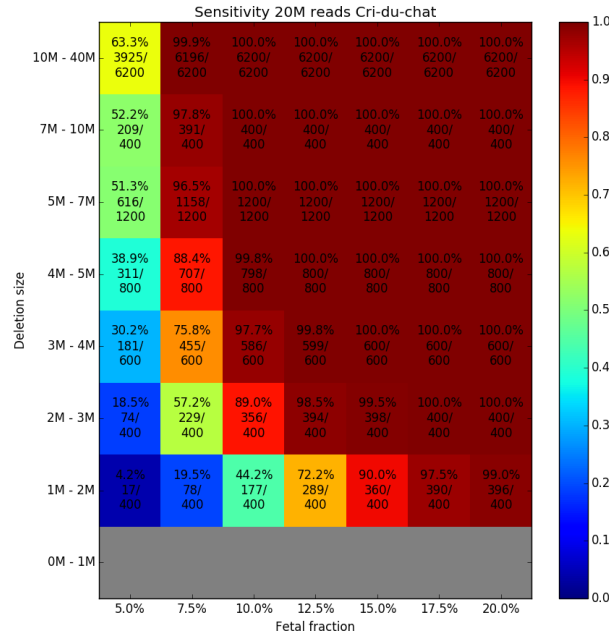
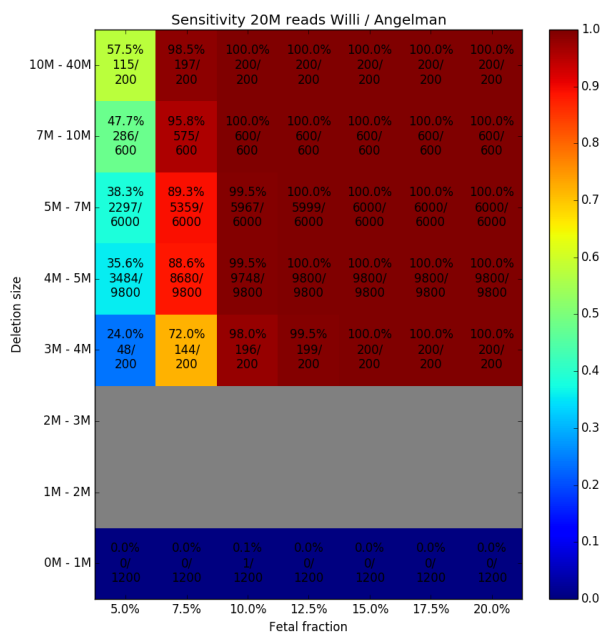
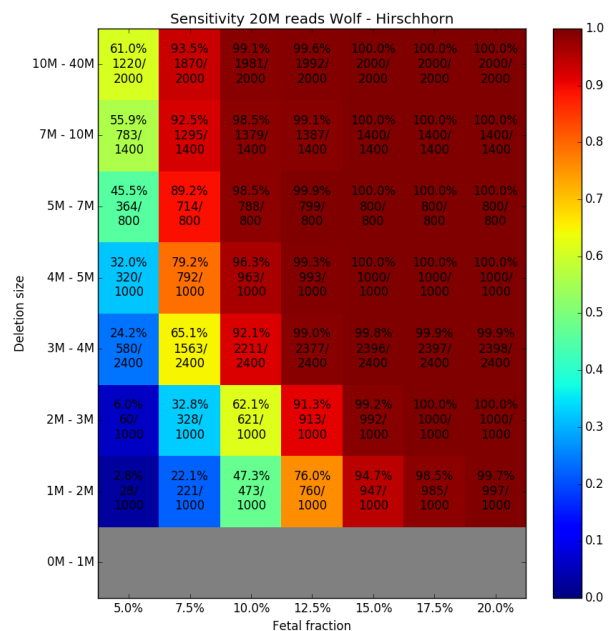
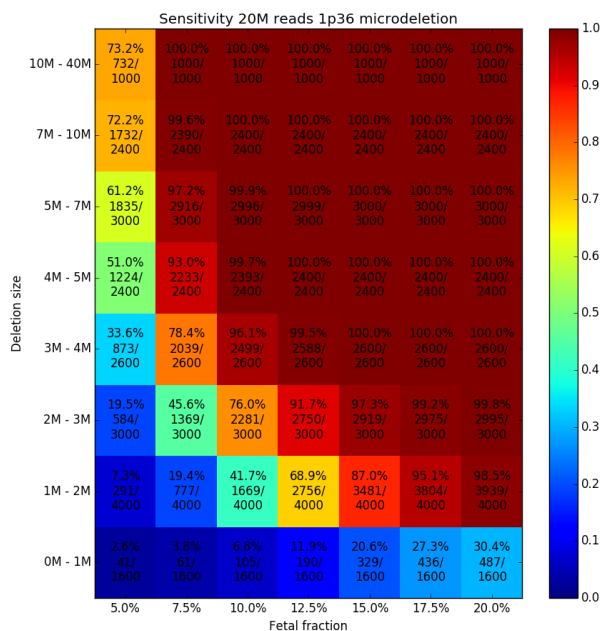


Fig H. Specificity of the prediction for different fetal fraction and microdeletion size.

Read count was set to 10M in each sample. Detections 2Mb away from critical region are NOT reported.



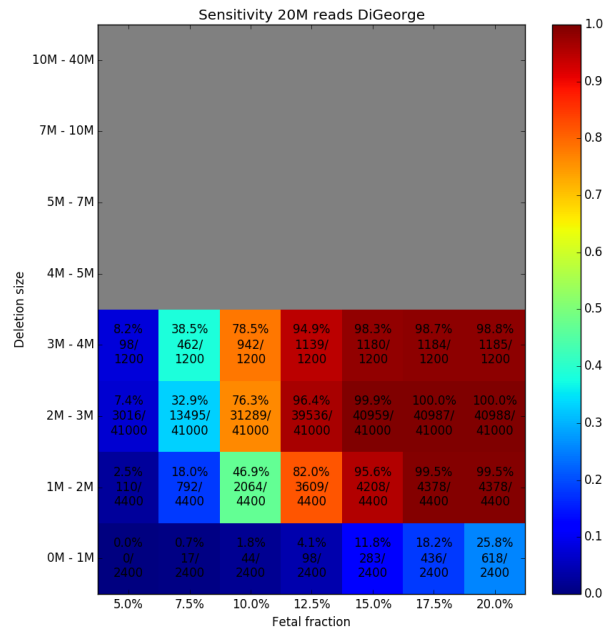


Fig I. Sensitivity of the prediction for different fetal fraction and size of microdeletion for different syndromes.

Read count was set to 20M in each sample. Detections 2M away from critical region are NOT reported.

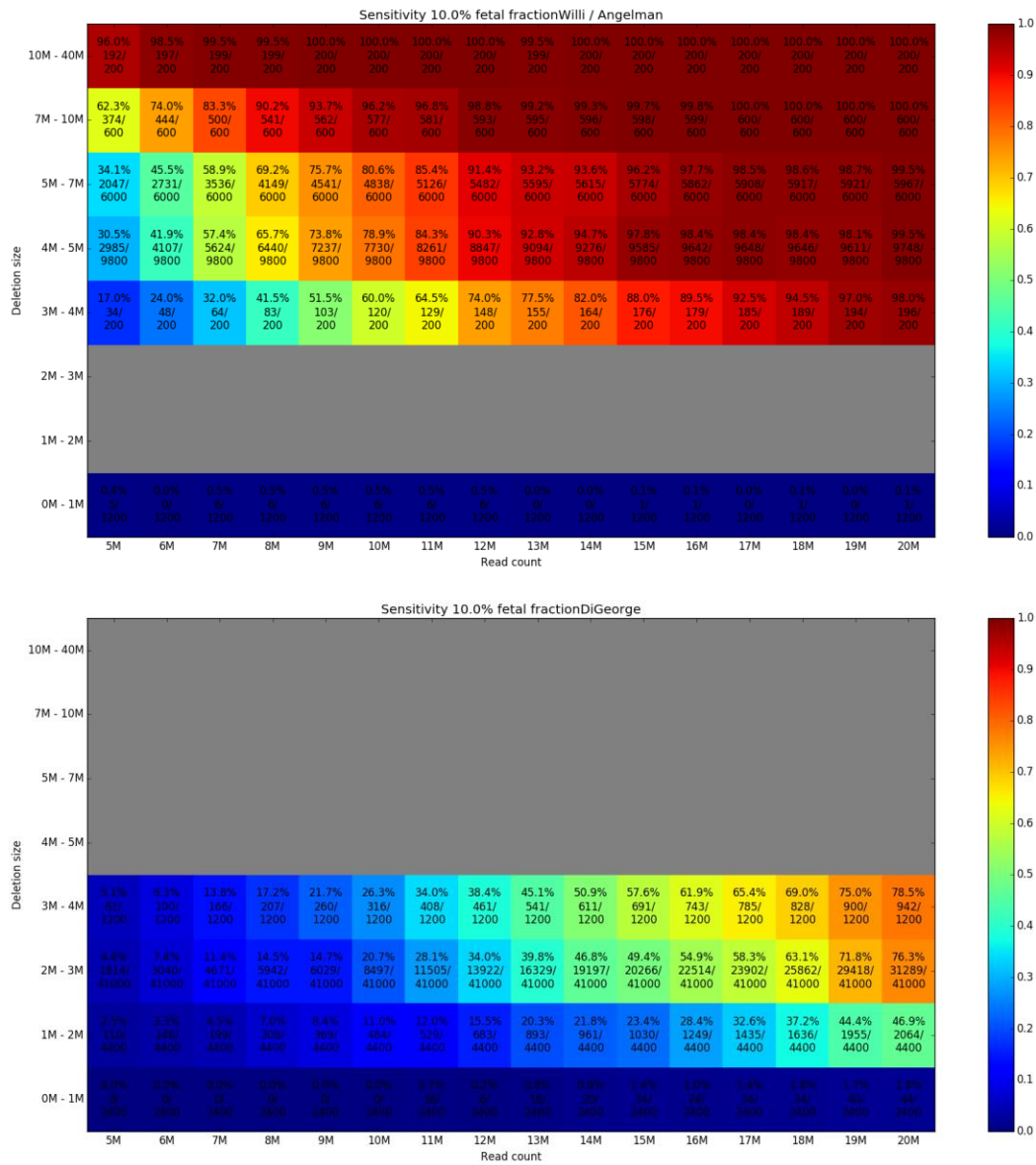


Fig J. Sensitivity of the prediction for different read count and microdeletion size.

Fetal fraction was set to 10% for all samples. Detections 2M away from critical region are NOT reported.

Table A. Detailed description of the control samples and their detection accuracy.

name	read count	fetal fraction	detection	local z score	size	syndrome
NA17942	17.5M	4.15%	ND	ND	2.6M	DiGeorge
BA161216	25.27M	4.50%	ND/grey zone	-2,48	3M	DiGeorge
NA22936	15.9M	4.86%	D	-5,28	21M	1p36 microdeletion
NA14124	16.47M	5.11%	D	-8,35	17.7M	Cri-du-chat
BA34	19.24M	5.90%	ND	ND	0.9M	DiGeorge
NA09024	15.3M	7.30%	D	-4,82	5.3M	Willi / Angelman
NA09024	12.66M	7.60%	D	-5,79	5.3M	Willi / Angelman
NA17942	19.6M	8.70%	D	-4,29	2.6M	DiGeorge
BA34	11M	8.80%	ND	ND	0.9M	DiGeorge
NA00072	8.3M	9.10%	D	-16,98	9.3M	Wolf - Hirschhorn
NA22936	21.5M	9.85%	D	-10,66	21M	1p36 microdeletion
NA11515	19.31M	10.60%	D	-5,59	6M	Willi / Angelman
BA34	9.9M	10%	ND	ND	0.9M	DiGeorge
BA161216	20.59M	11.20%	D	-4,71	3M	DiGeorge
BA34	20.36M	11.50%	D	-5,34	0.9M	DiGeorge
BA34	8.9M	11.99%	D	-5,74	0.9M	DiGeorge
NA11515	16.79M	12.20%	D	-9,02	6M	Willi / Angelman
NA09024	24.3M	13.40%	D	-7,38	5.3M	Willi / Angelman
NA11515	15.71M	13.90%	D	-9,54	6M	Willi / Angelman
NA00072	8.4M	14.10%	D	-14,62	9.3M	Wolf - Hirschhorn
NA09024	15.37M	14.50%	D	-10.25/-5.58	5.3M	Willi / Angelman
NA11515	19.26M	14.60%	D	-7,72	6M	Willi / Angelman
NA00072	16.2M	16.40%	D	-14,3	9.3M	Wolf - Hirschhorn
NA17942	14.5M	16.69%	D	-7,11	2.6M	DiGeorge
BA34	21.52M	17.30%	D	-6,52	0.9M	DiGeorge
NA17942	19.45M	17.30%	D	-6,71	2.6M	DiGeorge
BA161216	20.39M	20.10%	D	-8,27	3M	DiGeorge
NA17942	20.39M	20.10%	D	-8,27	2.6M	DiGeorge
NA09024	16.1M	20.50%	D	-13.50/-5.71	5.3M	Willi / Angelman

Table B. The number, mean size of pathogenic regions, and resulting critical regions, as reported by our study and DECIPHER database.

The number of pathogenic regions overlapping its corresponding critical region is reported in brackets. Finally, the number of pathogenic deletions from DECIPHER database that does not overlap ISCA database is low.

Identification of a syndrome		Number of pathogenic deletions		Mean size of pathogenic deletions	
Band	Name	ISCA	DECIPHER	ISCA	DECIPHER
1p36	1p36 deletion	102 (100)	54 (52)	4,131,271	3,174,263
4p16.3	Wolf-Hirschhorn	48 (48)	27 (27)	6,713,778	4,819,991
5p15	Cri-du-chat	50 (50)	24 (24)	14,887,247	8,873,724
15q11	Angelman / Prader-Willi	90 (90)	133 (133)	5,061,279	2,534,265
22q11.21	DiGeorge	280 (245)	136 (120)	2,368,692	2,444,038

Critical regions		Pathogenic deletions from DECIPHER not in ISCA critical region
ISCA	DECIPHER	
chr1: 564,424 - 21,598,492	chr1: 120,840 - 22,542,549	3
chr4: 85,040 - 2,010,761	chr4: 71,552 - 5,506,588	2
chr5: 1 - 15,678,560	chr5: 113,576 - 18,992,827	2
chr15: 22,779,922 - 28,559,437	chr15: 22,373,311 - 28,560,803	2
chr22: 18,661,724 - 21,505,417	chr22: 18,890,162 - 21,464,119	15